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OIPE

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/864,169

DATE: 06/08/2001
TIME: 16:45:24

Input Set : A:\208377.txt
Output Set: N:\CRF3\06082001\I864169.raw

ENTERED

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3 <110> APPLICANT: IMAEDA, TAKAO
4 YAMADA, YUKIO
5 HIRAI, MASANA
6 SHIMAMURA, TAKASHI
7 KOHDA, KATSUNORI
8 MURAMOTO, NOBUHIKO
10 <120> TITLE OF INVENTION: METHOD FOR PRODUCING ANTIMICROBIAL PROTEIN AND FUSION
PROTEIN
12 <130> FILE REFERENCE: 208377USO
C--> 14 <140> CURRENT APPLICATION NUMBER: US/09/864,169
C--> 14 <141> CURRENT FILING DATE: 2001-05-25
14 <150> PRIOR APPLICATION NUMBER: JP2000-161090
15 <151> PRIOR FILING DATE: 2000-05-26
17 <160> NUMBER OF SEQ ID NOS: 12
19 <170> SOFTWARE: PatentIn version 3.0
21 <210> SEQ ID NO: 1
22 <211> LENGTH: 392
23 <212> TYPE: DNA
24 <213> ORGANISM: Hordeum vulgare
26 <220> FEATURE:
27 <221> NAME/KEY: CDS
28 <222> LOCATION: (1)..(390)
30 <400> SEQUENCE: 1
31 gaa aag cat atg att gaa ggt cgt atg aaa agc tgc tgc cgt agc acc 48
32 Glu Lys His Met Ile Glu Gly Arg Met Lys Ser Cys Cys Arg Ser Thr
33 1 5 10 15
35 ctg ggt cgt aac tgc tat aac ctg tgc cgt gtt cgt ggt gcg cag aaa 96
36 Leu Gly Arg Asn Cys Tyr Asn Leu Cys Arg Val Arg Gly Ala Gln Lys
37 20 25 30
39 ctg tgc gcg ggt gtt tgc cgt tgc aaa ctg acc agc agc ggt aaa tgc 144
40 Leu Cys Ala Gly Val Cys Arg Cys Lys Leu Thr Ser Ser Gly Lys Cys
41 35 40 45
43 ccg acc ggt ttt ccg aaa atg att gaa ggt cgt acg ctg gcg ctg gtt 192
44 Pro Thr Gly Phe Pro Lys Met Ile Glu Gly Arg Thr Leu Ala Leu Val
45 50 55 60
47 agc aac agc gat gaa ccg gat acc gtt aaa tat tgc aac ctg ggt tgc 240
48 Ser Asn Ser Asp Glu Pro Asp Thr Val Lys Tyr Cys Asn Leu Gly Cys
49 65 70 75 80
51 cgt gcg agc atg tgc gat tat atg gtt aac gcg gcg gcg gat gat gaa 288
52 Arg Ala Ser Met Cys Asp Tyr Met Val Asn Ala Ala Ala Asp Asp Glu
53 85 90 95
55 gaa atg aaa ctg tat ctg gaa aac tgc ggt gat gcg tgc gtt aac ttt 336
56 Glu Met Lys Leu Tyr Leu Glu Asn Cys Gly Asp Ala Cys Val Asn Phe
57 100 105 110
59 tgc aac ggt gat gcg ggt ctg acc agc ctg acc gcg tga tag gat ccg 384
60 Cys Asn Gly Asp Ala Gly Leu Thr Ser Leu Thr Ala Asp Pro
61 115 120 125
63 gct gct aa 392

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64 Ala Ala
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69 <211> LENGTH: 124
70 <212> TYPE: PRT
71 <213> ORGANISM: Hordeum vulgare
73 <400> SEQUENCE: 2
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76 1 5 10 15
79 Leu Gly Arg Asn Cys Tyr Asn Leu Cys Arg Val Arg Gly Ala Gln Lys
80 20 25 30
83 Leu Cys Ala Gly Val Cys Arg Cys Lys Leu Thr Ser Ser Gly Lys Cys
84 35 40 45
87 Pro Thr Gly Phe Pro Lys Met Ile Glu Gly Arg Thr Leu Ala Leu Val
88 50 55 60
91 Ser Asn Ser Asp Glu Pro Asp Thr Val Lys Tyr Cys Asn Leu Gly Cys
92 65 70 75 80
95 Arg Ala Ser Met Cys Asp Tyr Met Val Asn Ala Ala Ala Asp Asp Glu
96 85 90 95
99 Glu Met Lys Leu Tyr Leu Glu Asn Cys Gly Asp Ala Cys Val Asn Phe
100 100 105 110
103 Cys Asn Gly Asp Ala Gly Leu Thr Ser Leu Thr Ala
104 115 120
107 <210> SEQ ID NO: 3
108 <211> LENGTH: 4
109 <212> TYPE: PRT
110 <213> ORGANISM: Hordeum vulgare
112 <400> SEQUENCE: 3
114 Asp Pro Ala Ala
115 1
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119 <211> LENGTH: 1649
120 <212> TYPE: DNA
121 <213> ORGANISM: Hordeum vulgare
123 <220> FEATURE:
124 <221> NAME/KEY: CDS
125 <222> LOCATION: (1)..(1647)
127 <400> SEQUENCE: 4
128 gac aag cat atg att gaa ggt cgt aaa agc tgc tgc cgt agc acc ctg 48
129 Asp Lys His Met Ile Glu Gly Arg Lys Ser Cys Cys Arg Ser Thr Leu
130 1 5 10 15
132 ggt cgt aac tgc tat aac ctg tgc cgt gtt cgt ggt gcg cag aaa ctg 96
133 Gly Arg Asn Cys Tyr Asn Leu Cys Arg Val Arg Gly Ala Gln Lys Leu
134 20 25 30
136 tgc gcg ggt gtt tgc cgt tgc aaa ctg acc agc agc ggt aaa tgc ccg 144
137 Cys Ala Gly Val Cys Arg Cys Lys Leu Thr Ser Ser Gly Lys Cys Pro
138 35 40 45
140 acc ggt ttt ccg aaa atg att gaa ggt cgt tcg gat gtt gtc cag ctg 192
141 Thr Gly Phe Pro Lys Met Ile Glu Gly Arg Ser Asp Val Val Gln Leu
142 50 55 60

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144	aag	aag	gac	acc	ttc	gac	gac	ttc	atc	aag	acg	aat	gac	ctt	gtt	ctc	240
145	Lys	Lys	Asp	Thr	Phe	Asp	Phe	Ile	Lys	Thr	Asn	Asp	Leu	Val	Leu		
146	65					70					75					80	
148	gcc	gaa	ttc	ttc	gcg	ccg	tgg	tgc	ggt	cac	tgc	aag	gct	ctc	gcc	ccc	288
149	Ala	Glu	Phe	Phe	Ala	Pro	Trp	Cys	Gly	His	Cys	Lys	Ala	Leu	Ala	Pro	
150					85					90					95		
152	gag	tac	gag	gag	gct	gcg	acc	aca	ctg	aag	gag	aag	aac	atc	aag	ctc	336
153	Glu	Tyr	Glu	Glu	Ala	Ala	Thr	Thr	Leu	Lys	Glu	Lys	Asn	Ile	Lys	Leu	
154					100					105					110		
156	gcc	aag	gtg	gac	tgc	aca	gag	gag	acg	gac	ctc	tgc	caa	caa	cat	ggt	384
157	Ala	Lys	Val	Asp	Cys	Thr	Glu	Glu	Thr	Asp	Leu	Cys	Gln	Gln	His	Gly	
158					115					120					125		
160	gtt	gag	ggc	tac	ccg	act	ctc	aag	gtc	ttc	cgc	ggc	ctt	gac	aac	gtc	432
161	Val	Glu	Gly	Tyr	Pro	Thr	Leu	Lys	Val	Phe	Arg	Gly	Leu	Asp	Asn	Val	
162					130					135					140		
164	tcc	ccc	tac	aag	ggc	cag	cgc	aag	gct	gct	gct	atc	acc	tcg	tac	atg	480
165	Ser	Pro	Tyr	Lys	Gly	Gln	Arg	Lys	Ala	Ala	Ala	Ile	Thr	Ser	Tyr	Met	
166	145					150									155		
168	atc	aag	cag	tct	ctg	ccc	gcc	gtg	tcc	gag	gtc	acg	aag	gac	aac	ctg	528
169	Ile	Lys	Gln	Ser	Leu	Pro	Ala	Val	Ser	Glu	Val	Thr	Gly	Asp	Asn	Leu	
170					165					170					175		
172	gag	gag	ttc	aag	aag	gcc	gac	aag	gcc	gtc	ctt	gtc	gcc	tat	gtg	gat	576
173	Glu	Glu	Phe	Lys	Lys	Ala	Asp	Lys	Ala	Val	Leu	Val	Ala	Tyr	Val	Asp	
174					180					185					190		
176	gct	tcc	gac	aag	gcg	tcc	agt	gag	gtt	ttc	acc	cag	gtc	gcc	gag	aag	624
177	Ala	Ser	Asp	Lys	Ala	Ser	Ser	Glu	Val	Phe	Thr	Gln	Val	Ala	Glu	Lys	
178					195					200					205		
180	ctg	cgc	gac	aac	tac	ccg	ttc	ggc	tcc	agc	agc	gat	gct	gcg	ctg	gcc	672
181	Leu	Arg	Asp	Asn	Tyr	Pro	Phe	Gly	Ser	Ser	Ser	Asp	Ala	Ala	Leu	Ala	
182					210					215					220		
184	gag	gct	gag	ggc	gtc	aag	gct	ccc	gct	atc	gtc	ctt	tac	aag	gac	ttt	720
185	Glu	Ala	Glu	Gly	Val	Lys	Ala	Pro	Ala	Ile	Val	Leu	Tyr	Lys	Asp	Phe	
186	225					230									235		
188	gat	gag	ggc	aag	gcg	gtc	ttc	tcc	gag	aag	ttc	gag	gtg	gag	gcg	atc	768
189	Asp	Glu	Gly	Lys	Ala	Val	Phe	Ser	Glu	Lys	Phe	Glu	Val	Glu	Ala	Ile	
190					245					250					255		
192	gag	aag	ttc	gcc	aag	acg	ggc	gcc	acc	ccg	ctc	att	ggc	gag	att	ggc	816
193	Glu	Lys	Phe	Ala	Lys	Thr	Gly	Ala	Thr	Pro	Leu	Ile	Gly	Glu	Ile	Gly	
194					260					265					270		
196	ccc	gaa	acc	tac	tcc	gac	tac	atg	tcg	gcc	ggc	atc	cct	ctg	gcc	tac	864
197	Pro	Glu	Thr	Tyr	Ser	Asp	Tyr	Met	Ser	Ala	Gly	Ile	Pro	Leu	Ala	Tyr	
198					275					280					285		
200	att	ttc	gcc	gaa	acg	gcc	gag	gag	cgg	aag	gag	ctc	agc	gac	aag	ctc	912
201	Ile	Phe	Ala	Glu	Thr	Ala	Glu	Glu	Arg	Lys	Glu	Leu	Ser	Asp	Lys	Leu	
202					290					295					300		
204	aag	ccg	atc	gcc	gag	gct	cag	cgc	ggc	gtc	att	aac	ttt	ggt	act	att	960
205	Lys	Pro	Ile	Ala	Glu	Ala	Gln	Arg	Gly	Val	Ile	Asn	Phe	Gly	Thr	Ile	
206	305					310									315		
208	gac	gcc	aag	gct	ttt	ggt	gcc	cac	gcc	ggc	aac	ctg	aac	ctg	aag	acc	1008

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209 Asp Ala Lys Ala Phe Gly Ala His Ala Gly Asn Leu Asn Leu Lys Thr
210          325          330          335
212 gac aag ttc ccc gcc ttc gcc atc cag gag gtc gcc aag aac cag aag      1056
213 Asp Lys Phe Pro Ala Phe Ala Ile Gln Glu Val Ala Lys Asn Gln Lys
214          340          345          350
216 ttc ccc ttc gat cag gag aag gag atc acc ttc gag gcg atc aag gct      1104
217 Phe Pro Phe Asp Gln Glu Lys Glu Ile Thr Phe Glu Ala Ile Lys Ala
218          355          360          365
220 ttc gtc gac gac ttt gtc gcc ggt aag atc gag ccc agc atc aag tcg      1152
221 Phe Val Asp Asp Phe Val Ala Gly Lys Ile Glu Pro Ser Ile Lys Ser
222          370          375          380
224 gag ccg atc cct gag aag cag gag gcc ccc gtc acc gtc gtc gtt gcc      1200
225 Glu Pro Ile Pro Glu Lys Gln Glu Gly Pro Val Thr Val Val Val Ala
226 385          390          395          400
228 aag aac tac aat gag atc gtc ctg gac gac acc aag gat gtg ctg att      1248
229 Lys Asn Tyr Asn Glu Ile Val Leu Asp Asp Thr Lys Asp Val Leu Ile
230          405          410          415
232 gag ttc tac gcc ccg tgg tgc gcc cac tgc aag gcc ctg gct ccc aag      1296
233 Glu Phe Tyr Ala Pro Trp Cys Gly His Cys Lys Ala Leu Ala Pro Lys
234          420          425          430
236 tac gag gag etc gcc gcc ctg tat gcc aag agc gag ttc aag gac cgg      1344
237 Tyr Glu Glu Leu Gly Ala Leu Tyr Ala Lys Ser Glu Phe Lys Asp Arg
238          435          440          445
240 gtc gtc atc gcc aag gtt gat gcc acg gcc aac gac gtt ccc gat gag      1392
241 Val Val Ile Ala Lys Val Asp Ala Thr Ala Asn Asp Val Pro Asp Glu
242          450          455          460
244 atc cag gga ttc ccc acc atc aag ctg tac ccg gcc ggt gcc aag ggt      1440
245 Ile Gln Gly Phe Pro Thr Ile Lys Leu Tyr Pro Ala Gly Ala Lys Gly
246 465          470          475          480
248 cag ccc gtc acc tac tct gcc tcg cgc act gtc gag gac ctc atc aag      1488
249 Gln Pro Val Thr Tyr Ser Gly Ser Arg Thr Val Glu Asp Leu Ile Lys
250          485          490          495
252 ttc atc gcc gag aac gcc aag tac aag gcc gcc atc tcg gag gat gcc      1536
253 Phe Ile Ala Glu Asn Gly Lys Tyr Lys Ala Ala Ile Ser Glu Asp Ala
254          500          505          510
256 gag gag acg tcg tcc gca acc gag acg acc acc gag acg gcc acc aag      1584
257 Glu Glu Thr Ser Ser Ala Thr Glu Thr Thr Thr Glu Thr Ala Thr Lys
258          515          520          525
260 tcg gag gag gct gcc aag gag acg gcg acg gag cac gac gag etc tga      1632
261 Ser Glu Glu Ala Ala Lys Glu Thr Ala Thr Glu His Asp Glu Leu
262          530          535          540
264 tag gat ccg gct gct aa      1649
265 Asp Pro Ala Ala
266          545
269 <210> SEQ ID NO: 5
270 <211> LENGTH: 543
271 <212> TYPE: PRT
272 <213> ORGANISM: Hordeum vulgare
274 <400> SEQUENCE: 5

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Input Set : A:\208377.txt
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276 Asp Lys His Met Ile Glu Gly Arg Lys Ser Cys Cys Arg Ser Thr Leu
277 1 5 10 15
280 Gly Arg Asn Cys Tyr Asn Leu Cys Arg Val Arg Gly Ala Gln Lys Leu
281 20 25 30
284 Cys Ala Gly Val Cys Arg Cys Lys Leu Thr Ser Ser Gly Lys Cys Pro
285 35 40 45
288 Thr Gly Phe Pro Lys Met Ile Glu Gly Arg Ser Asp Val Val Gln Leu
289 50 55 60
292 Lys Lys Asp Thr Phe Asp Asp Phe Ile Lys Thr Asn Asp Leu Val Leu
293 65 70 75 80
296 Ala Glu Phe Phe Ala Pro Trp Cys Gly His Cys Lys Ala Leu Ala Pro
297 85 90 95
300 Glu Tyr Glu Glu Ala Ala Thr Thr Lys Glu Lys Asn Ile Lys Leu
301 100 105 110
304 Ala Lys Val Asp Cys Thr Glu Glu Thr Asp Leu Cys Gln Gln His Gly
305 115 120 125
308 Val Glu Gly Tyr Pro Thr Leu Lys Val Phe Arg Gly Leu Asp Asn Val
309 130 135 140
312 Ser Pro Tyr Lys Gly Gln Arg Lys Ala Ala Ala Ile Thr Ser Tyr Met
313 145 150 155 160
316 Ile Lys Gln Ser Leu Pro Ala Val Ser Glu Val Thr Lys Asp Asn Leu
317 165 170 175
320 Glu Glu Phe Lys Lys Ala Asp Lys Ala Val Leu Val Ala Tyr Val Asp
321 180 185 190
324 Ala Ser Asp Lys Ala Ser Ser Glu Val Phe Thr Gln Val Ala Glu Lys
325 195 200 205
328 Leu Arg Asp Asn Tyr Pro Phe Gly Ser Ser Ser Asp Ala Ala Leu Ala
329 210 215 220
332 Glu Ala Glu Gly Val Lys Ala Pro Ala Ile Val Leu Tyr Lys Asp Phe
333 225 230 235 240
336 Asp Glu Gly Lys Ala Val Phe Ser Glu Lys Phe Glu Val Glu Ala Ile
337 245 250 255
340 Glu Lys Phe Ala Lys Thr Gly Ala Thr Pro Leu Ile Gly Glu Ile Gly
341 260 265 270
344 Pro Glu Thr Tyr Ser Asp Tyr Met Ser Ala Gly Ile Pro Leu Ala Tyr
345 275 280 285
348 Ile Phe Ala Glu Thr Ala Glu Glu Arg Lys Glu Leu Ser Asp Lys Leu
349 290 295 300
352 Lys Pro Ile Ala Glu Ala Gln Arg Gly Val Ile Asn Phe Gly Thr Ile
353 305 310 315 320
356 Asp Ala Lys Ala Phe Gly Ala His Ala Gly Asn Leu Asn Leu Lys Thr
357 325 330 335
360 Asp Lys Phe Pro Ala Phe Ala Ile Gln Glu Val Ala Lys Asn Gln Lys
361 340 345 350
364 Phe Pro Phe Asp Gln Glu Lys Glu Ile Thr Phe Glu Ala Ile Lys Ala
365 355 360 365
368 Phe Val Asp Asp Phe Val Ala Gly Lys Ile Glu Pro Ser Ile Lys Ser
369 370 375 380
372 Glu Pro Ile Pro Glu Lys Gln Glu Gly Pro Val Thr Val Val Val Ala

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VERIFICATION SUMMARY

PATENT APPLICATION: US/09/864,169

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Input Set : A:\208377.txt

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L:14 M:270 C: Current Application Number differs, Replaced Current Application No

L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date